IFW

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/527,552
Source: PCT
Date Processed by STIC: 12/08/2005

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PCT

RAW SEQUENCE LISTING DATE: 12/08/2005
PATENT APPLICATION: **US/10/527,552** TIME: 10:41:00

Input Set : **A:\32677_sequence listing.txt**
Output Set: **N:\CRF4\12082005\J527552.raw**

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      3 <110> APPLICANT: Sandoz GmbH
      5 <120> TITLE OF INVENTION: Process for production of cephalosporin C
      7 <130> FILE REFERENCE: IB/G-32677A/BCK
C-->  9 <140> CURRENT APPLICATION NUMBER: US/10/527,552
C--> 10 <141> CURRENT FILING DATE: 2005-03-11
     12 <160> NUMBER OF SEQ ID NOS: 21
     14 <170> SOFTWARE: PatentIn version 3.2
     16 <210> SEQ ID NO: 1
     17 <211> LENGTH: 526
     18 <212> TYPE: PRT
     19 <213> ORGANISM: Acremonium chrysogenum
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     28             20                  25                  30
     31 Phe Pro Asn Gly Ser Tyr Ile Gly Trp Ser Gly Phe Thr Gly Val Gly
     32         35                  40                  45
     35 Tyr Pro Lys Lys Met Pro Thr Tyr Met Ala Asp His Val Glu Gln Asn
     36     50                  55                  60
     39 Gly Leu Gln Gly Lys Leu Lys Tyr Ser Leu Phe Val Gly Ala Ser Ser
     40 65                  70                  75                  80
     43 Gly Ala Glu Thr Glu Asn Arg Trp Ala Ser Leu Asp Met Ile Asp Arg
     44                 85                  90                  95
     47 Arg Thr Pro His Gln Val Gly Lys Ala Ile Ser Lys Gly Ile Asn Glu
     48             100                 105                 110
     51 Gly Lys Ile His Phe Phe Asp Lys His Leu Ser Met Phe Pro Val Asp
     52         115                 120                 125
     55 Leu Val Tyr Gly Tyr Tyr Thr Lys Asp Arg Pro His Asn Lys Leu Asp
     56     130                 135                 140
     59 Val Val Val Val Glu Ala Thr Asp Ile Lys Glu Asp Gly Ser Ile Val
     60 145                 150                 155                 160
     63 Pro Gly Ala Ser Val Gly Ala Thr Pro Glu Leu Ile Gln Met Ala Asp
     64                 165                 170                 175
     67 Lys Ile Ile Ile Glu Val Asn Thr Ser Leu Pro Ser Phe Glu Gly Leu
     68             180                 185                 190
     71 His Asp Ile Thr Met Thr Asp Leu Pro Pro Leu Arg Lys Pro Tyr Leu
     72         195                 200                 205
     75 Val Met Gly Val Glu Asp Arg Ile Gly Arg Thr Ser Ile Pro Ile Asp
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     80 225                 230                 235                 240
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88             260                 265                 270
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95 Ile Gly Gly Leu Asp Asn Ser Asn Phe Arg Asn Leu Lys Val Trp Thr
96     290                 295                 300
99 Glu Val Ile Gln Asp Thr Phe Leu Asp Leu Phe Asp Ser Gly Arg Leu
100 305                 310                 315                 320
103 Asp Phe Ala Thr Ala Thr Ser Ile Arg Phe Ser Pro Asp Gly Phe Arg
104                 325                 330                 335
107 Arg Phe Tyr Asp Asn Trp Glu Ala Tyr Tyr Gly Lys Leu Leu Leu Arg
108             340                 345                 350
111 Ser Gln Gln Val Ser Asn Ser Pro Glu Ile Ile Arg Arg Leu Gly Val
112         355                 360                 365
115 Ile Ala Met Asn Thr Pro Val Glu Val Asp Ile Tyr Ala His Ala Asn
116     370                 375                 380
119 Ser Thr Cys Val Met Gly Ser Arg Met Leu Asn Gly Leu Gly Gly Ser
120 385                 390                 395                 400
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124                 405                 410                 415
127 Thr Arg Pro Ser Lys Thr Asp Pro His Gly Val Ser Cys Ile Val Pro
128             420                 425                 430
131 Met Cys Thr His Ile Asp Gln Thr Glu His Asp Leu Asp Val Ile Val
132         435                 440                 445
135 Thr Glu Gln Gly Leu Ala Asp Val Arg Gly Leu Ser Pro Arg Glu Arg
136     450                 455                 460
139 Ala Arg Val Ile Ile Lys Lys Cys Ala His Pro Val Tyr Gln Pro Ile
140 465                 470                 475                 480
143 Leu Thr His Tyr Phe Glu Lys Ala Glu Ser Asp Cys Leu Arg Lys Gly
144                 485                 490                 495
147 Trp Gly His Glu Pro His Leu Leu Phe Asn Ser Phe Asp Leu His Lys
148             500                 505                 510
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157 <212> TYPE: DNA
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165 tggtccggct tcaccggcgt cggctacccg aagtgagttc caccgtcatc ccgctccaca    180
167 gtaggcgcag ccggcccgct gacagtcccc gacaggaaaa tgccgaccta catggccgat    240
169 cacgtcgagc agaacggcct tcagggcaag ctgaagtact cgctattcgt gggcgcatcg    300
171 tcgggtgctg agacagagaa tcgctgggcg tcgctcgaca tgattgatag gaggaccccg    360
173 catcaggtcg gcaaggccat ctccaagggc atcaatgagg gcaagatcca cttcttcgac    420
175 aagcatctct ccatgttccc cgtggacctt gtatacgtac gtcaacgatg atcccttgga    480
177 atgtgcatgt actacgagta cctggcgcta acatccggtc agggctacta cacaaaggat    540
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183 gtgagcaatt tcgatttcta gcggagggcg cagcaggacc tgacatctcc ctgtgcagat    720
185 cattatcgag gtcaacacct cactgccttc attcgagggt ctccacgaca tcaccatgac    780
187 cgacctgccc ccgctacgga agccctatct cgtcatgggt gtcgaggacc gcatcggcag    840
189 gacctctatc cctatcgacc ccgagaaggt tgtaggcatc ctcgaatccg actaccagga    900
191 cgccactgcc cccaacgccg aggccgacga gagtgcgaac aagattgctg gccacttgat    960
193 tgagttcttc gagcacgagg tcgcccacgg ccgtctcccg aactccctcc ttcccctcca   1020
195 gtccggcatc ggcaacgtcg ccaacgccat catcggtggc ctcgacaact ccaacttccg   1080
197 caacctcaag gtctggactg aggttatcca ggacaccttc ctcgacctct tcgactcggg   1140
199 ccgcctcgac tttgccacgg ccacctctat ccgcttctcc cccgacggtt tccgccggtt   1200
201 ctacgacaac tgggaggcct actacggcaa gctcctcctc cgcagccagc aggtgtccaa   1260
203 ctcgcccgag atcatccgcc gccttggtgt cattgccatg aacacccccg tcgaggtcga   1320
205 catctacgcc cacgccaact ccacctgcgt catgggctcg cgcatgctca acggcctggg   1380
207 cggctccgcc gacttcctgc gctcctccaa gtactctatc atgcacaccc cgtccacccg   1440
209 cccctccaag accgacccgc acggcgtctc gtgcatcgtt cccatgtgca cccacatcga   1500
211 ccagactgag cacgacctcg acgtcatcgt caccgagcag ggcctggccg acgtgcgcgg   1560
213 cctgagcccc agggagaggg cccgcgtcat catcaagaag tgcgcccacc cggtctacca   1620
215 gcccatcctg acccactact ttgagaaggc cgagagcgac tgcctacgca agggctgggg   1680
217 ccacgagccc catctgctct tcaactcgtt tgacctgcac aaggccctcg tggagcacgg   1740
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224 <212> TYPE: DNA
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232 tggtccggct tcaccggcgt cggctacccg aagaaaatgc cgacctacat ggccgatcac    180
234 gtcgagcaga acggccttca gggcaagctg aagtactcgc tattcgtggg cgcatcgtcg    240
236 ggtgctgaga cagagaatcg ctgggcgtcg ctcgacatga ttgataggag gaccccgcat    300
238 caggtcggca aggccatctc caagggcatc aatgagggca agatccactt cttcgacaag    360
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242 aacaagctgg acgtggtggt ggtggaggcc accgacatca aagaggacgg aagcattgta    480
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248 cccccgctac ggaagcccta tctcgtcatg ggtgtcgagg accgcatcgg caggacctct    660
250 atccctatcg accccgagaa ggttgtaggc atcctcgaat ccgactacca ggacgccact    720
252 gcccccaacg ccgaggccga cgagagtgcg aacaagattg ctggccactt gattgagttc    780
254 ttcgagcacg aggtcgccca cggccgtctc ccgaactccc tccttccctt ccagtccggc    840
256 atcggcaacg tcgccaacgc catcatcggt ggcctcgaca actccaactt ccgcaacctc    900
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264 gagatcatcc gccgccttgg tgtcattgcc atgaacaccc ccgtcgaggt cgacatctac   1140
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270 aagaccgacc cgcacggcgt ctcgtgcatc gttcccatgt gcacccacat cgaccagact   1320
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276 ctgacccact actttgagaa ggccgagagc gactgcctac gcaagggctg gggccacgag 1500
278 ccccatctgc tcttcaactc gtttgacctg cacaaggccc tcgtggagca cggaagcatg 1560
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293 atgcgatact atggcgtggc gtggggtcgc gtcggtgtcc ggccggtcga acggaggtcc 180
295 cggctatcaa taggcggtag gccggcattg aatcggttcc accgtattcc agacacccaa 240
297 ggaaggcccg ccacccccag ctccggcctg gggatagcgc cgagtggagc actcacgggg 300
299 gccgtgtttg actcgaagac gcgtcgtgat tggccagaac ttcatccccc tctgccaagt 360
301 attggttcac gggattcggc gacgtcaacg accccaccgg cccggattac ataaggtgca 420
303 ctgcagctac tacgtagtac tcgtacttgg gaaggaggga cccttggggt cggaggtttt 480
305 aaaggcaatg gcttcttcgc tggtccaccc aacctgactc tcactctccc ttttacctcg 540
307 ctcctctgat tattccctcg tctgcgtctg gatttcatct ctttcccctc ccggcccctt 600
309 tggatctctg ctctcccctc ctctctcccc cgcattggtg tgtaaaacca ctgtcccgcg 660
311 gcctcgcgac gagtgacgta ctgcaagccg aaacctcaca atcccttcct cacaatggca 720
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317 ggcttcaccg gcgtcggcta cccgaagtga gttccaccgt catcccgctc cacagtaggc 900
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384 <222> LOCATION: (15909)..(15909)
385 <223> OTHER INFORMATION: n is a, c, g, or t
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394 ttgctggtgg tttaacatag ccggcaaggg gaaaaaaaaa agggggcgga gaaggactga    240
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458 cgggccatcg cgcttggccg aggagagaaa gggtatccat ggcgacaaag gcggtcctgg   2160
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 15909

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:8,9,10,11,12,13,14,15,16,17,18,19,20,21

VERIFICATION SUMMARY DATE: 12/08/2005
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Input Set : **A:\32677_sequence listing.txt**
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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:918 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:15900